

Reviewer Report

Title: An integrated chromosome-scale genome assembly of the Masai Giraffe (*Giraffa camelopardalis tippelskirchi*)

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Reviewer Comments to Author:

The manuscript is about resequencing the genome of the Masai Giraffe and constructing a high quality and contiguity chromosome-level reference assembly for the species. The goal was to improve over the previous assembly (Agaba et al. 2016), so that the resulting genome sequence would be applicable for evolutionary studies and species conservation. The authors used a well-selected set of cutting-edge next generation genomics technologies (short- and long-read sequencing; proximity ligation sequencing) and bioinformatics tools to achieve the goal. The manuscript is very well written and clear.

However, while reading the manuscript, I was very positive and enthusiastic in the beginning but disappointed in the end. To me, the manuscript looked like a well-written and detailed methodological manual about how to generate a high-quality chromosome-level annotated genome assembly for any mammalian species. I could recommend it for this purpose to any graduate student and postdoc. Disappointment was because I learned very little about the Masai Giraffe as such. Maybe this was the intention of the authors and in accordance with the profile of the journal. If so, this is a beautiful methodological paper on how to sequence, assemble and annotate mammalian genomes. If not, the authors should provide more information specific to the species.

Specific comments:

1. Like any other re-sequencing project, the manuscript should provide a comparison with the previous assembly together with examples illustrating the improvement (filling gaps or improving gene models, etc.).
2. It would be worth mentioning that together with the study by Agaba et al., there are now sequences of 3 female Masai Giraffe genomes.
3. The authors mention in Introduction about the specific biological features and adaptations of the Masai Giraffe, but do not use the improved sequence assembly to show this. If genome-wide analysis of signatures of selection is a too big task (and it likely is), the authors should revisit the genes under selection as pointed out by Agaba et al. (2016), and demonstrate how the new assembly improves this information.
4. The authors mention in Introduction about the use of the assembly for conservation efforts of the giraffe but do not show in the manuscript how it will be done.
5. Fig. 1: please specify whether this is the photo of the sequenced individual or just a representative of a species

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